SEQUENCE LISTING

<110> ACHEN, Marc G.
STACKER, Steven A.

<120> METHODS FOR TREATING NEOPLASTIC DISEASE CHARACTERIZED BY VASCULAR ENDOTHELIAL GROWTH FACTOR D EXPRESSION, FOR SCREENING FOR NEOPLASTIC DISEASE OR METASTATIC RISK AND FOR MAINTAINING VASCULARIZATION OF TISSUE

<130> 1064/48666PC

<140> to be assigned
<141> 2001-09-20

<150> 09/796,714
<151> 2001-03-02

<150> 60/234,196
<151> 2000-09-20

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<170> PatentIn version 3.1

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ttagagtgct ttctaatttc aggtagaaga catgtccacc ttctgattat ttttggagaa 180

cattttgatt tttttcatct ctctctcccc acccctaaga ttgtgcaaaa aaagcgtacc 240

ttgcctaatt gaaataattt cattggattt tgatcagaac tgattatttg gttttctgtg 300

tgaagttttg aggtttcaaa ctttccttct ggagaatgcc ttttgaaaca attttctcta 360

gctgcctgat gtcaactgct tagtaatcag tggatattga aatattcaaa atg tac 416
Met Tyr
1

aga gag tgg gta gtg gtg aat gtt ttc atg atg ttg tac gtc cag ctg 464
Arg Glu Trp Val Val Val Asn Val Phe Met Met Leu Tyr Val Gln Leu
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Val Gln Gly Ser Ser Asn Glu His Gly Pro Val Lys Arg Ser Ser Gln
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tcc aca ttg gaa cga tct gaa cag cag atc agg gct gct tct agt ttg      560
Ser Thr Leu Glu Arg Ser Glu Gln Gln Ile Arg Ala Ala Ser Ser Leu
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gag gaa cta ctt cga att act cac tct gag gac tgg aag ctg tgg aga      608
Glu Glu Leu Leu Arg Ile Thr His Ser Glu Asp Trp Lys Leu Trp Arg
                55                  60                  65

tgc agg ctg agg ctc aaa agt ttt acc agt atg gac tct cgc tca gca      656
Cys Arg Leu Arg Leu Lys Ser Phe Thr Ser Met Asp Ser Arg Ser Ala
            70                  75                  80

tcc cat cgg tcc act agg ttt gcg gca act ttc tat gac att gaa aca      704
Ser His Arg Ser Thr Arg Phe Ala Ala Thr Phe Tyr Asp Ile Glu Thr
        85                  90                  95

cta aaa gtt ata gat gaa gaa tgg caa aga act cag tgc agc cct aga      752
Leu Lys Val Ile Asp Glu Glu Trp Gln Arg Thr Gln Cys Ser Pro Arg
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gaa acg tgc gtg gag gtg gcc agt gag ctg ggg aag agt acc aac aca      800
Glu Thr Cys Val Glu Val Ala Ser Glu Leu Gly Lys Ser Thr Asn Thr
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ttc ttc aag ccc cct tgt gtg aac gtg ttc cga tgt ggt ggc tgt tgc      848
Phe Phe Lys Pro Pro Cys Val Asn Val Phe Arg Cys Gly Gly Cys Cys
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aat gaa gag agc ctt atc tgt atg aac acc agc acc tcg tac att tcc      896
Asn Glu Glu Ser Leu Ile Cys Met Asn Thr Ser Thr Ser Tyr Ile Ser
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aaa cag ctc ttt gag ata tca gtg cct ttg aca tca gta cct gaa tta      944
Lys Gln Leu Phe Glu Ile Ser Val Pro Leu Thr Ser Val Pro Glu Leu
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gtg cct gtt aaa gtt gcc aat cat aca ggt tgt aag tgc ttg cca aca      992
Val Pro Val Lys Val Ala Asn His Thr Gly Cys Lys Cys Leu Pro Thr
    180                 185                 190

gcc ccc cgc cat cca tac tca att atc aga aga tcc atc cag atc cct     1040
Ala Pro Arg His Pro Tyr Ser Ile Ile Arg Arg Ser Ile Gln Ile Pro
195                 200                 205                 210

gaa gaa gat cgc tgt tcc cat tcc aag aaa ctc tgt cct att gac atg     1088
Glu Glu Asp Arg Cys Ser His Ser Lys Lys Leu Cys Pro Ile Asp Met
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cta tgg gat agc aac aaa tgt aaa tgt gtt ttg cag gag gaa aat cca     1136
Leu Trp Asp Ser Asn Lys Cys Lys Cys Val Leu Gln Glu Glu Asn Pro
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ctt gct gga aca gaa gac cac tct cat ctc cag gaa cca gct ctc tgt     1184
Leu Ala Gly Thr Glu Asp His Ser His Leu Gln Glu Pro Ala Leu Cys
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ggg cca cac atg atg ttt gac gaa gat cgt tgc gag tgt gtc tgt aaa     1232
Gly Pro His Met Met Phe Asp Glu Asp Arg Cys Glu Cys Val Cys Lys
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aca cca tgt ccc aaa gat cta atc cag cac ccc aaa aac tgc agt tgc     1280
Thr Pro Cys Pro Lys Asp Leu Ile Gln His Pro Lys Asn Cys Ser Cys
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ttt gag tgc aaa gaa agt ctg gag acc tgc tgc cag aag cac aag cta     1328
Phe Glu Cys Lys Glu Ser Leu Glu Thr Cys Cys Gln Lys His Lys Leu
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ttt cac cca gac acc tgc agc tgt gag gac aga tgc ccc ttt cat acc     1376
Phe His Pro Asp Thr Cys Ser Cys Glu Asp Arg Cys Pro Phe His Thr
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aga cca tgt gca agt ggc aaa aca gca tgt gca aag cat tgc cgc ttt     1424
Arg Pro Cys Ala Ser Gly Lys Thr Ala Cys Ala Lys His Cys Arg Phe
        325                 330                 335

cca aag gag aaa agg gct gcc cag ggg ccc cac agc cga aag aat cct     1472
Pro Lys Glu Lys Arg Ala Ala Gln Gly Pro His Ser Arg Lys Asn Pro
    340                 345                 350

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ccttttgttt agttttgttt ttgtttttg gtgaatgaga aaggtgtgct ggtcatggaa   1772

tggcaggtgt catatgactg attactcaga gcagatgagg aaaactgtag tctctgagtc   1832

ctttgctaat cgcaactctt gtgaattatt ctgattcttt tttatgcaga atttgattcg   1892

tatgatcagt actgactttc tgattactgt ccagcttata gtcttccagt ttaatgaact   1952

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Ser Gln Ser Thr Leu Glu Arg Ser Glu Gln Gln Ile Arg Ala Ala Ser
        35                  40                  45
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Ser Leu Glu Glu Leu Leu Arg Ile Thr His Ser Glu Asp Trp Lys Leu
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Trp Arg Cys Arg Leu Arg Leu Lys Ser Phe Thr Ser Met Asp Ser Arg
65 70 75 80

Ser Ala Ser His Arg Ser Thr Arg Phe Ala Ala Thr Phe Tyr Asp Ile
85 90 95

Glu Thr Leu Lys Val Ile Asp Glu Glu Trp Gln Arg Thr Gln Cys Ser
100 105 110

Pro Arg Glu Thr Cys Val Glu Val Ala Ser Glu Leu Gly Lys Ser Thr
115 120 125

Asn Thr Phe Phe Lys Pro Pro Cys Val Asn Val Phe Arg Cys Gly Gly
130 135 140

Cys Cys Asn Glu Glu Ser Leu Ile Cys Met Asn Thr Ser Thr Ser Tyr
145 150 155 160

Ile Ser Lys Gln Leu Phe Glu Ile Ser Val Pro Leu Thr Ser Val Pro
165 170 175

Glu Leu Val Pro Val Lys Val Ala Asn His Thr Gly Cys Lys Cys Leu
180 185 190

Pro Thr Ala Pro Arg His Pro Tyr Ser Ile Ile Arg Arg Ser Ile Gln
195 200 205

Ile Pro Glu Glu Asp Arg Cys Ser His Ser Lys Lys Leu Cys Pro Ile
210 215 220

Asp Met Leu Trp Asp Ser Asn Lys Cys Lys Cys Val Leu Gln Glu Glu
225 230 235 240

Asn Pro Leu Ala Gly Thr Glu Asp His Ser His Leu Gln Glu Pro Ala
245 250 255

Leu Cys Gly Pro His Met Met Phe Asp Glu Asp Arg Cys Glu Cys Val
260 265 270

Cys Lys Thr Pro Cys Pro Lys Asp Leu Ile Gln His Pro Lys Asn Cys
275 280 285

Ser Cys Phe Glu Cys Lys Glu Ser Leu Glu Thr Cys Cys Gln Lys His
290 295 300

Lys Leu Phe His Pro Asp Thr Cys Ser Cys Glu Asp Arg Cys Pro Phe
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His Thr Arg Pro Cys Ala Ser Gly Lys Thr Ala Cys Ala Lys His Cys
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Arg Phe Pro Lys Glu Lys Arg Ala Ala Gln Gly Pro His Ser Arg Lys
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Asn Pro

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35 40 45

Arg Cys Gly Gly Cys Cys Asn Glu Glu Ser Leu Ile Cys Met Asn Thr
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Ser Thr Ser Tyr Ile Ser Lys Gln Leu Phe Glu Ile Ser Val Pro Leu
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ttccatgtgt acttggtgca gggcttcagg agcgaacatg gaccagtgaa ggatttttct 180

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tttgcggcaa ctttctatga cactgaaaca ctaaaagtta tagatgaaga atggcagagg 420

acccaatgca gccctagaga gacatgcgta gaagtcgcca gtgagctggg gaagacaacc 480

aacacattct tcaagccccc ctgtgtaaat gtcttccggt gtggaggctg ctgcaacgaa 540

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tgtaagtgct tgcccacggg cccccgccat ccttactcaa ttatcagaag atccattcag 720

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ctaag 1325